



SEQUENCE LISTING

<110> Buechler, Joe
Valkirs, Gunars
Gray, Jeff
Lonberg, Nils
Biosite Diagnostics, Inc.
GenPharm International

<120> Human Antibodies

<130> 020015-000110US

<140> 09/453,234

<141> 1999-12-01

<150> US 60/157,415

<151> 1999-10-02

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<170> PatentIn Ver. 2.1

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43

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<213> Artificial Sequence

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43

<210> 4

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.<212> DNA
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<400> 7
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<213> Artificial Sequence

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<210> 9
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.<213> Artificial Sequence

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46

<210> 10

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo 935

<400> 10

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46

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<211> 46

<212> DNA

<213> Artificial Sequence

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<400> 11

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46

<210> 12

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo 937

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46

<210> 13

<211> 46

<212> DNA

<213> Artificial Sequence

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<400> 13

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<210> 14

<211> 46

<212> DNA

<213> Artificial Sequence

<220>
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46

<210> 15
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<212> DNA
<213> Artificial Sequence

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21

<210> 16
<211> 43
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<223> Description of Artificial Sequence: Oligo 945

<400> 16
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43

<210> 17
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 946

<400> 17
ttacccctgt ggcaaaagcc gaggtgcagc tggcagtc tgg

43

<210> 18
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 947

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43

<210> 19
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<213> Artificial Sequence

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<400> 19
gacagatggt gcagccacag t 21

<210> 20
<211> 75
<212> DNA
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<400> 20
atctggcaca tcatatggat aagttcgtg tacaaaatgc cagacctaga ggaattttat 60
ttccagcttg gtccc 75

<210> 21
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo 862

<400> 21
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ggtgactga 69

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 5

<400> 22
gcaactgttg ggaaggg 17

<210> 23
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: Primer 197

<400> 23
tcgctgcccc accagccatg 20

<210> 24
<211> 46
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 869

<400> 24
gggaccaagc tggaaataaa acgggctgtg gctgcaccat ctgtct

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<210> 25
<211> 45
<212> DNA
<213> Artificial Sequence

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<400> 25
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45

<210> 26
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 867

<400> 26
tcagtcaccg tctcctcagc ctccaccaag ggcccatc

38

<210> 27
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 876

<400> 27
gtgatggtga tggtgatgag atttgggctc tgctttcttg tcc

43

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 885

<400> 28
taagagcggt aagagtgc当地 g

21

<210> 29
<211> 69
<212> DNA
<213> Artificial Sequence

.<220>
<223> Description of Artificial Sequence: Primer 970

<400> 29
gtgataaaact accgtaaagc ttatcgatga taagctgtca attagtgtatg gtgatggta 60
tgagatttg 69

<210> 30
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 17 Decapeptide

<400> 30
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

<210> 31
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Example 19
Primer A

<400> 31
tcgctgcccc accagccatg gccagtgcta aagaacttag atctcag 47

<210> 32
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Example 19
Primer B

<400> 32
gtgataaaact accgcattaa agcttatcga tgataagctg tcaatttagtg atggatgg 60
tgatgtaat tctcagccct cttcaa 86

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Example 19
Primer C

<400> 33
gcaactctct actgtttctc c 21

.<210> 34
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Example 19
 Primer D

<400> 34
 gaggatgacg atgagcgc

18

<210> 35
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
 <223> M1-1L

<400> 35
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 ctctcctgca gggccagtca ggggtttagc agctacttag cctggtagcca acagaaacct 120
 gggcaggctc ccaggtctt catctatgtat gcatccaaca gggccactgg catcccagcc 180
 aggttcagtg gcagtggttc tgggacagac ttcaactctca ccatcagcag cctagagcct 240
 gaagattttt cagtttatta ctgtcagcag cgtagcaact ggcctcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgaactgtg gctgcacccat ctgtcttcat cttcccgcca 360
 tctgtatgagc agttgaaatc tggaaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaagggtg gataacgccc tccaatcggg taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtac ccatcaggc 600
 ctgagctcgc cctgtcacaaa gagcttcaac aggggagagt cttatccata tgatgtgcca 660
 gattatgcga gc 672

<210> 36
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 36
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100	105	110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser		
210	215	220

<210> 37
 <211> 678
 <212> DNA
 <213> Homo sapiens

<220>
 <223> M1-3L

<220>
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<400> 37
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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

cca ttc act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg 336
 Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
 100 105 110

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc
 Ala Ser
 225

<210> 38
 <211> 226
 <212> PRT
 <213> Homo sapiens
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<400> 38
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
 225

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<223> M1-4L

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 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc cac 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu His
 35 40 45

atc tat ggt gca tcc aga agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag ttt ggt agc tca ttc	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Phe	
85 90 95	
act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca	336
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
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 <213> Homo sapiens
 <223> M1-4L

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20 25 30	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu His	
35 40 45	
Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 41
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<220>
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 <222> (1)...(678)

<220>
 <223> M1-5L

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

'ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	
ata ttc act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg	336
Ile Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val	
100 105 110	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa	384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys	
115 120 125	
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac	480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn	
145 150 155 160	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa	576
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys	
180 185 190	
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca	624
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr	
195 200 205	
aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat	672
Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr	
210 215 220	
gcg agc	678
Ala Ser	
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<210> 42
<211> 226
<212> PRT
<213> Homo sapiens
<223> M1-5L

<400> 42
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Ile Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
 225

<210> 43
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc acc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt	192	
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser		
50 55 60		
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu		
65 70 75 80		
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca ttc	288	
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe		
85 90 95		
act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca	336	
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala		
100 105 110		
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384	
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115 120 125		
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432	
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130 135 140		
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480	
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145 150 155 160		
gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc	528	
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165 170 175		
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576	
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180 185 190		
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624	
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195 200 205		
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672	
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser		
210 215 220		
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<211> 224		
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<213> Homo sapiens		
<223> M1-8L		
<400> 44		
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly		
1 5 10 15		
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr		
20 25 30		
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu		

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 45

<211> 672

<212> DNA

<213> Homo sapiens

<220>

<223> M1-10L

<220>

<221> CDS

<222> (1)...(672)

<400> 45

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 Asp Val Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc	192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	
agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	
gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccc	288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro	
85 90 95	
act ttc ggc gga ggg acc aag gtg gag atc aaa cga act gtg gct gca	336
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
210 215 220	

<210> 46
 <211> 224
 <212> PRT
 <213> Homo sapiens
 <223> M1-10L

<400> 46
 Asp Val Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 47
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> (1)...(672)

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 Ala Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tat 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

'tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt gtc 192
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Val
 50 55 60

agt gga tct ggg aca gat ctc act ctc acc atc agc agt ctg caa cct 240
 Ser Gly Ser Gly Thr Asp Leu Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

gaa gat ttt gca act tat tac tgt cag tgt tac agt aca cca ttc 288
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Tyr Ser Thr Pro Phe
 85 90 95

act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384
 Pro Ser Val Phe Ile Phe Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

agc acc ctg acg ctg agc, aaa gca gac tac gag aaa cac aaa gtc tac 576
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 48

<211> 224

<212> PRT

<213> Homo sapiens

<223> M1-21L

<400> 48

Ala Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Val
 50 55 60

Ser Gly Ser Gly Thr Asp Leu Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Tyr Ser Thr Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 49

<211> 678

<212> DNA

<213> Homo sapiens

<220>

<223> M1-23L

<220>

<221> CDS

<222> (1) .. (678)

<400> 49

gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192

' Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 336
 Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

gag gcc aaa gta cag tgg agg gtg gat aac gcc ctc caa tcg ggt aac 480
 Glu Ala Lys Val Gln Trp Arg Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc 678
 Ala Ser
 225

<210> 50
 <211> 226
 <212> PRT
 <213> Homo sapiens
 <223> M1-23L

<400> 50
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Arg Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
 225

<210> 51
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
 <223> M1-25L

<400> 51
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 ctctcctgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaaa 120
 cctggccagg ctcccaggct cctcatctat ggtcatcca gcagggccac tggcatccca 180
 aacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag cagatggta gctcattcac tttcgccct 300
 gggaccaaaat tggatataa acgaactgtg gctgcaccat ctgtcttcattt cttcccgcca 360
 tctgtatgagc agttgaaatc tggaaactgcc tctgttgtgt gcctgtgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaagggtg gataacgccc tccaatcggtt taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac agggagagt cttatccata tgatgtgcc 660

'gattatgcga gc

672

<210> 52

<211> 224

<212> PRT

<213> Homo sapiens

<220>

<223> M1-25L

<400> 52

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asn Arg Phe Ser
50 55 60Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe
85 90 95Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Asn
210 215 220

<210> 53

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<223> M1-1H

<220>

<221> CDS

<222> (1)..(675)

<400> 53

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	aag	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys	
1	5			10								15				

tcc	ctg	aga	ctc	tcc	tgt	gca	gcf	tct	gaa	ttc	acc	atc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Glu	Phe	Thr	Ile	Ser	Tyr	Tyr	
20			25									30				

ggc	atg	cac	tgg	gtc	cgc	cag	gtt	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35			40								45					

gca	gct	gtc	tgg	tat	gat	gaa	agt	act	aca	tat	tct	cca	gac	tcc	gtg	192
Ala	Ala	Val	Trp	Tyr	Asp	Glu	Ser	Thr	Thr	Tyr	Ser	Pro	Asp	Ser	Val	
50			55								60					

aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	gat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	
65			70							75			80			

ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85			90							95						

gcg	aga	gat	agg	gtg	ggc	ctc	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Arg	Val	Gly	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
100			105							110						

gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
115			120							125						

gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys
130			135							140						

ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145			150						155			160				

ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	528
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
165			170							175						

tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	576
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
180			185							190						

ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	624
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
195			200							205						

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 54
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 <213> Homo sapiens
 <223> M1-1H

<400> 54
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Ile Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ala Val Trp Tyr Asp Glu Ser Thr Thr Tyr Ser Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 55
 <211> 677
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> (3) .. (677)

<400> 55

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 Asp Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly
 1 5 10 15

agg tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac 95
 Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr
 20 25 30

tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg 143
 Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45

gtg aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc 191
 Val Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser
 50 55 60

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 239
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 65 70 75

tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac 287
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 80 85 90 95

tgt gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc 335
 Cys Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc 383
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc 431
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac 479
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155

tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag 527
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 160 165 170 175

tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc 575

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Val Thr Val Pro Ser Ser
 180 185 190

agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc 623
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

aac acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac 671
 Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His
 210 215 220

cat cac 677
 His His
 225

<210> 56
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M1-3H

<400> 56
 Asp Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 57
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
 <223> M1-4H

<220>
 <221> CDS
 <222> (1) .. (675)

<400> 57

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	aag	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys	
1	5			10								15				

tcc	ctg	aga	ctc	tcc	tgt	gca	gcg	tct	gga	ttc	acc	ttc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Tyr	Tyr	
20			25									30				

ggc	atg	cac	tgg	gtc	cgc	cag	gtt	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35			40								45					

gca	gct	gtc	tgg	tat	gat	gga	agt	act	aca	tat	tct	cca	gac	tcc	gtg	192
Ala	Ala	Val	Trp	Tyr	Asp	Gly	Ser	Thr	Thr	Tyr	Ser	Pro	Asp	Ser	Val	
50			55								60					

aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	gat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	
65			70								75		80			

ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85			90								95					

gcg	aga	gat	agg	gtg	ggc	ctc	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Arg	Val	Gly	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
100			105								110					

gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
115			120								125					

gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
130			135								140					

ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145			150								155		160			

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528	
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser		
165	170	175
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576	
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser		
180	185	190
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624	
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn		
195	200	205
acc aag gtg gac aag aaa gca ggg ccc aaa tct cat cac cat cac cat	672	
Thr Lys Val Asp Lys Lys Ala Gly Pro Lys Ser His His His His His		
210	215	220
cac	675	
His		
225		

<210> 58

<211> 225

<212> PRT

<213> Homo sapiens

<223> M1-4H

<400> 58

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Lys			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr			
20	25	30	

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	

Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val			
50	55	60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr			
65	70	75	80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu			
115	120	125	

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys			
130	135	140	

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser			
145	150	155	160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser			
165	170	175	

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Gly Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 59

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<223> M1-5H

<220>

<221> CDS

<222> (1)...(675)

<400> 59

cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg 48
 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192
 Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 60
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M1-5H

<400> 60
 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 61
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
 <223> M1-8H

<220>
 <221> CDS
 <222> (1)...(675)

<400> 61
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 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys
 1 5 10 15

tcc ctg aaa ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat 96
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gct gta tgg tat gat gga agt aac aca tac tct cca gac tcc gtg 192
 Ala Ala Val Trp Tyr Asp Gly Ser Asn Thr Tyr Ser Pro Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg gtg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg		384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu		
115	120	125
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc		432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys		
130	135	140
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca		480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser		
145	150	155
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc		528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser		
165	170	175
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc		576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser		
180	185	190
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac		624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn		
195	200	205
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat		672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His		
210	215	220
cac		675
His		
225		
<210> 62		
<211> 225		
<212> PRT		
<213> Homo sapiens		
<223> M1-8H		
<400> 62		
Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys		
1	5	10
15		
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr		
20	25	30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ala Ala Val Trp Tyr Asp Gly Ser Asn Thr Tyr Ser Pro Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr		
65	70	75
80		
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu		
100	105	110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 63

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<223> M1-10H

<220>

<221> CDS

<222> (1) .. (708)

<400> 63

cag gtg cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Gln Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gaa ggc tct gga ttc atc ttc agg aac cat 96
 Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His
 20 25 30

cct ata cac tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca gtt agt ggt att ggt ggt gac aca tac tat gca gac tcc gtg aag 192
 Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc tcc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga gaa tat tac tat ggt tcg ggg agt tat cgc gtt gac tac tac tac 336
 Arg Glu Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr
 100 105 110

tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca 384
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag 432
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 130 135 140

agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac 480
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 145 150 155 160

ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc 528
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 165 170 175

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc 576
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 180 185 190

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc 624
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 195 200 205

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag 672
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 210 215 220

aaa gca gag ccc aaa tct cat cac cat cac cat cac 708
 Lys Ala Glu Pro Lys Ser His His His His His His
 225 230 235

<210> 64
 <211> 236
 <212> PRT
 <213> Homo sapiens
 <223> M1-10H

<400> 64
 Gln Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His
 20 25 30

Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Glu Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr
 100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 130 135 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 145 150 155 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 165 170 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 180 185 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 195 200 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 210 215 220

Lys Ala Glu Pro Lys Ser His His His His His
 225 230 235

<210> 65

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<223> M1-21H

<220>

<221> CDS

<222> (1)..(675)

<400> 65

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 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg agc agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg	336
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

<210> 66
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M1-21H

<400> 66
 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 67
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> (1)...(675)

<400> 67
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 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt aac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gct ata tgg tat gat gga agt aaa aca tac aat gca gac tcc gtg 192
 Ala Ala Ile Trp Tyr Asp Gly Ser Lys Thr Tyr Asn Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gat ggg ata ggc tac ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 68
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M1-23H

<400> 68
 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ala Ile Trp Tyr Asp Gly Ser Lys Thr Tyr Asn Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 69
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> (1)..(675)

<400> 69
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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt tac tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr	
20 25 30	
ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtc	144
Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
gca gct gtc tgg tat gat gga agt act aca tat cct cca gac tcc gtc	192
Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Pro Pro Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtt tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg	336
Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

<210> 70
 <211> 225
 <212> PRT

<213> Homo sapiens
 <223> M1-25H

<400> 70
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Pro Pro Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220
 His
 225

<210> 71
 <211> 678
 <212> DNA
 <213> Homo sapiens
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 <222> (1)...(678)
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<223> M2-11L

<400> 71
 gaa ata gtg atg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag ggt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

cca ttc act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg 336
 Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
 100 105 110

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aga 384
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Arg
 115 120 125

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc 678
 Ala Ser

225

<210> 72
 <211> 226
 <212> PRT
 <213> Homo sapiens
 <223> M2-11L

<400> 72
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Arg
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser

225

<210> 73
 <211> 678
 <212> DNA
 <213> Homo sapiens

<220>
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<222> (1) . . (678)

<220>
<223> M2-12L

<400> 73
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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

 gaa aga gcc acc ctc tcc tgc agg gcc agt cag ggt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
 20 25 30

 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

 atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

 ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

 cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

 ccg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 336
 Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

 tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

 gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc 678
 Ala Ser
 225

<210> 74
 <211> 226
 <212> PRT
 <213> Homo sapiens
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<400> 74
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
 225

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<210> 75
<211> 672
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) .. (672)

<220>
<223> M2-16L

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Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc	96	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser		
20	25	30

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tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
            35           40           45

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atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
      50          55          60

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gtc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Val Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
   65           70           75           80

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cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ttc 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe
 85 90 95

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act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca 336
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
                     100          105          110

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  cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384
  Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
  115          120          125

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act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	432
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	
	130				135						140					

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aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145           150           155           160

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gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc 528
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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180

185

190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 76
 <211> 224
 <212> PRT
 <213> Homo sapiens
 <223> M2-16L

<400> 76
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Val Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 77
 <211> 672
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(672)

 <220>
 <223> M2-18L

 <400> 77

gaa ata gtg atg acg cag tct cca ggc acc ctg tct ttg tct cca ggg	48
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc acc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca ttc	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe	
85 90 95	
act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct gca	336
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
210 215 220	
<210> 78	
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<212> PRT	
<213> Homo sapiens	
<223> M2-18L	
<400> 78	
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1 5 10 15	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr	
20 25 30	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe	
85 90 95	
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala	
100 105 110	
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
210 215 220	

<210> 79
 <211> 678
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (678)

<220>
 <223> M2-20L

<400> 79 48
 gaa ata gtg atg acg cag tct cca ggc acc ctg tct ttg tct cca ggg
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 atc tac ggt gca tcc agg agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ccc 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 atg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 336
 Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110
 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125
 tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140
 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160
 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc 678
 Ala Ser
 225

<210> 80
 <211> 226
 <212> PRT
 <213> Homo sapiens
 <223> M2-20L

<400> 80
 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
225

<210> 81
 <211> 672
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(672)

 <220>
 <223> M2-31L

 <400> 81

gaa att gtg ttg acg cag tct cca gcc acc ctg tct ttg tct cca ggg	48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr	
20 25 30	
tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc	144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile	
35 40 45	
tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc	192
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	
agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	
gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg	288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg	
85 90 95	
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca	336
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga	384
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc	432
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
. 130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag	480
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	

165

170

175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac 576
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672
 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 82
 <211> 224
 <212> PRT
 <213> Homo sapiens
 <223> M2-31L

<400> 82
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 83
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(672)

<220>
 <223> M2-32L

<400> 83
 gaa att gtg ttg acg cag tct cca gcc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

tat gat gca tcc aac agg gcc gct ggc atc cca gcc agg ttc agt ggc 192
 Tyr Asp Ala Ser Asn Arg Ala Ala Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag caa cgt aac aac tgg cct ctc 288
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Asn Trp Pro Leu
 85 90 95

act ttc ggc gga ggg acc aag gtg gag atc aaa cga act gtg gct gca 336
 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

act gcc tct gtt gtg tgc ctg aat aac ttc tat ccc aga gag gcc 432
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc 528
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
210 215 220	
<210> 84	
<211> 224	
<212> PRT	
<213> Homo sapiens	
<223> M2-32L	
<400> 84	
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr	
20 25 30	
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile	
35 40 45	
Tyr Asp Ala Ser Asn Arg Ala Ala Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Asn Trp Pro Leu	
85 90 95	
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	

210

215

220

<210> 85
<211> 678
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1) .. (678)

<220>
<223> M2-33L

<400> 85
gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45
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atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
   65          70          75          80

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cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 336
 Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

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gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
          115          120          125

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tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga	432
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg	
130 135 140	

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gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145           150           155           160

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tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc	528
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser	
165 170 175	

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 624
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205

aag agc ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat 672
 Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

gcg agc 678
 Ala Ser
 225

<210> 86

<211> 226

<212> PRT

<213> Homo sapiens

<223> M2-33L

<400> 86

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
 100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr

195

200

205

Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr
 210 215 220

Ala Ser
 225

<210> 87
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(672)

<220>
 <223> M2-34L

<400> 87
 gaa att gtg ttg acg cag tct cca gcc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg 288
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg
 85 90 95

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca 336
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc 432
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145	150	155	160	
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser				528
165	170	175		
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr				576
180	185	190		
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser				624
195	200	205		
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser				672
210	215	220		
<210> 88				
<211> 224				
<212> PRT				
<213> Homo sapiens				
<223> M2-34L				
<400> 88				
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly				
1	5	10	15	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr				
20	25	30		
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile				
35	40	45		
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly				
50	55	60		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro				
65	70	75	80	
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg				
85	90	95		
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala				
100	105	110		
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly				
115	120	125		
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala				
130	135	140		
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln				
145	150	155	160	
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser				
165	170	175		
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr				
180	185	190		

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 89
 <211> 672
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(672)

<220>
 <223> M2-35L

<400> 89
 gaa att gtg ttg acg cag tct cca gcc acc ctg tct ttg tct cca ggg 48
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag cgt acg aac tgg cct cgg 288
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg
 85 90 95

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca 336
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga 384
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

act gcc tct gtt gtg tgc ctg aat aac ttc tat ccc aga gag gcc 432
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag 480
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

gag agt gtc aca gag cag gac aag gac agc acc tac agc ctc agc	528
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac	576
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc	624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	
195 200 205	
ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc	672
Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
210 215 220	

<210> 90

<211> 224

<212> PRT

<213> Homo sapiens

<223> M2-35L

<400> 90

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr	
20 25 30	

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile	
35 40 45	

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly	
50 55 60	

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro	
65 70 75 80	

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg	
85 90 95	

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	
100 105 110	

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	
115 120 125	

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	
130 135 140	

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	
145 150 155 160	

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	
165 170 175	

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	
180 185 190	

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 210 215 220

<210> 91
 <211> 675
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 <213> Homo sapiens

<220>
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 <222> (1) .. (675)

<220>
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<400> 91
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 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192
 Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528																																
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser																																	
165	170	175		tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576	Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser		180	185	190		ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624	Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn		195	200	205		acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672	Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His		210	215	220		cac	675	His		225	
175																																	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576																																
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser																																	
180	185	190		ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624	Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn		195	200	205		acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672	Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His		210	215	220		cac	675	His		225									
190																																	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624																																
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn																																	
195	200	205		acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672	Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His		210	215	220		cac	675	His		225																	
205																																	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672																																
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His																																	
210	215	220		cac	675	His		225																									
220																																	
cac	675																																
His																																	
225																																	

<210> 92

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-11H

<400> 92

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg			
1	5	10	15
10	15		

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr			
20	25	30	
30			

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
45			

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val			
50	55	60	
60			

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
75	80		

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
95			

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	
110			

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu			
115	120	125	
125			

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys			
130	135	140	
140			

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser			
145	150	155	160
155	160		

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser			
165	170	175	
175			

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
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<210> 93

<211> 675

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)...(675)

<220>

<223> M2-12H

<400> 93

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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gaa tgg atg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

aca ctt ata tcc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192
 Thr Leu Ile Ser Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gaa aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys

130

135

140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc agc 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Ser
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 94
 <211> 225
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Thr Leu Ile Ser Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Ser
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 95
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1) .. (675)

<220>
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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc agc ttg agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg tgg 144
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gct gtc tgg tat gat gga agt act aga tat tct cca gac tcc gtg 192
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Arg Tyr Ser Pro Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

<210> 96

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-16H

<400> 96

Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys	
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Tyr Tyr	
20 25 30	

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

Ala Ala Val Trp Tyr Asp Gly Ser Thr Arg Tyr Ser Pro Asp Ser Val	
50 55 60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr	
65 70 75 80	

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu	
100 105 110	

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 97

<211> 675

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(675)

<220>

<223> M2-18H

<400> 97

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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc agc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192
 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Ser Pro Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

gct gac gat agg gtc ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gct gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Thr Ala Ala Leu Gly Cys
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtc acg gtc tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtc gtc acc gtc ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtc aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtc gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 98
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M2-18H

<400> 98
 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 99
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1) .. (675)

<220>
 <223> M2-20H

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 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

tcc ctg agg ctc tcc tgt gca gcc tct gga ttc act ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggg atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtc 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ctt ata aca tat gat gga agg aat aaa tac tac gcc gac tcc gtc 192
 Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gag aat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga act gag gac acg gct gag tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Glu Tyr Tyr Cys	
85 90 95	
gcu aga gac ggg atc gga tac ttt gac tac tgg ggc cag gga atc ctg	336
Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Ile Leu	
100 105 110	
gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	384
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
115 120 125	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	432
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	
130 135 140	
ctg gtg aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aag tca	480
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Lys Ser	
145 150 155 160	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	528
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
165 170 175	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	576
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
180 185 190	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	624
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
195 200 205	
acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat	672
Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His	
210 215 220	
cac	675
His	
225	

<210> 100

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-20H

<400> 100

Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Glu Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Ile Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Lys Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220
 His
 225

<210> 101
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg 144
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

gca ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg 192
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 102
 <211> 225
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 <213> Homo sapiens
 <223> M2-31H

<400> 102
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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

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<220>
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 <222> (1)...(708)

<220>
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<400> 103
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 1 5 10 15

tcc ctg aga ctc tcc tgt gaa ggc tct gga ttc atc ttc agg aac cat	96
Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His	
20 25 30	
cct ata cac tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca gtt agt ggt att ggt ggt gac aca tac tat gca gac tcc gtg aag	192
Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc tcc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga gaa tat tac tat ggt tcg ggg agt tat cgc gtt gac tac tac tac	336
Arg Glu Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr	
100 105 110	
tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca	384
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	
gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag	432
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys	
130 135 140	
agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac	480
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr	
145 150 155 160	
ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc	528
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
165 170 175	
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc	576
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
180 185 190	
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc	624
Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr	
195 200 205	
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag	672
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	
210 215 220	
aaa gca gag ccc aaa tct cat cac cat cac cat cac	708
Lys Ala Glu Pro Lys Ser His His His His His His	
225 230 235	

<210> 104

<211> 236

<212> PRT

<213> Homo sapiens

<223> M2-32H

<400> 104
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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His
 20 25 30
 Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Glu Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr
 100 105 110
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 130 135 140
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 145 150 155 160
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 165 170 175
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 180 185 190
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 195 200 205
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 210 215 220
 Lys Ala Glu Pro Lys Ser His His His His His His
 225 230 235

<210> 105
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(675)

<220>
 <223> M2-33H

<400> 105
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 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttt acc ttc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gaa tgg atg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

aca ctt ata acc tat gat gga gat aat aaa tac tat gca gac tcc gtg 192
 Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac ggg atc ggg tac ttt gac tat tgg ggc cag gga acc ctg 336
 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 106
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M2-33H

<400> 106
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 107
 <211> 675
 <212> DNA
 <213> Homo sapiens

<220>
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<222> (1)..(675)

<220>
<223> M2-34H

<400> 107

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Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1			5				10					15				

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acg	ttc	agt	tac	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Tyr	Tyr	
20				25								30				

ggt	ata	cac	tgg	gtc	cgc	cag	gtt	cca	ggc	aag	gga	cta	gag	tgg	gtg	144
Gly	Ile	His	Trp	Val	Arg	Gln	Val	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35					40					45						

gta	ctt	ata	tca	tac	gat	gga	agc	aat	aaa	tac	tac	gca	gac	tcc	gtg	192
Val	Leu	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
50					55				60							

aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	act	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65				70					75			80				

ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85					90					95						

gcg	aga	gac	tgg	atc	ggg	tac	ttt	gac	tac	tgg	ggc	cag	gga	acc	ctg	336
Ala	Arg	Asp	Trp	Ile	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	
100					105					110						

gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	384
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
115					120					125						

gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	432
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
130					135					140						

ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	480
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
145					150					155			160			

ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	528
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
165					170					175						

tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	576
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
180					185					190						

ctg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	624
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
195					200					205						

acc	aag	gtg	gac	aag	aaa	gca	gag	ccc	aaa	tct	cat	cac	cat	cac	cat	672
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 108
 <211> 225
 <212> PRT
 <213> Homo sapiens
 <223> M2-34H

<400> 108
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Val Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

His
 225

<210> 109
 <211> 675
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(675)

 <220>
 <223> M2-35H

 <400> 109
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 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg atc agt tac tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Tyr Tyr
 20 25 30

 ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg 144
 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 gaa ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg 192
 Glu Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg 336
 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc 432
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

 ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

 tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat 672
 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His
 210 215 220

cac 675
 His
 225

<210> 110
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 <212> PRT
 <213> Homo sapiens
 <223> M2-35H

<400> 110
 Gln Val Gin Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg 15
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Tyr Tyr
 20 25 30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Glu Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His

210

215

220

His
225<210> 111
<211> 70
<212> DNA
<213> Artificial Sequence<220>
<223> Description of Artificial Sequence: Figure 2 Kappa Chain<400> 111
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70
tggaggcttg<210> 112
<211> 70
<212> DNA
<213> Artificial Sequence<220>
<223> Description of Artificial Sequence: Figure 2 Heavy Chain<400> 112
tgagggttcct tgaccccaact gcagagttACT aggctctGA gctactcAGT taggtgattG 60
70
agttagccAGT